Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:59:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013312.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6013312 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013312.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:59:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013312.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,396,288
Mapped reads	1,267,175 / 90.75%
Unmapped reads	129,113 / 9.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,104 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	53,894 / 3.86%
Duplication rate	3.53%
Clipped reads	641,277 / 45.93%

2.2. ACGT Content

Number/percentage of A's	22,519,432 / 27.3%
Number/percentage of C's	15,064,199 / 18.26%
Number/percentage of T's	26,336,917 / 31.93%
Number/percentage of G's	18,552,781 / 22.49%
Number/percentage of N's	9,656 / 0.01%
GC Percentage	40.76%

2.3. Coverage

Mean	0.0267

Standard Deviation	0.2457

2.4. Mapping Quality

Mean Mapping Quality	45.63

2.5. Mismatches and indels

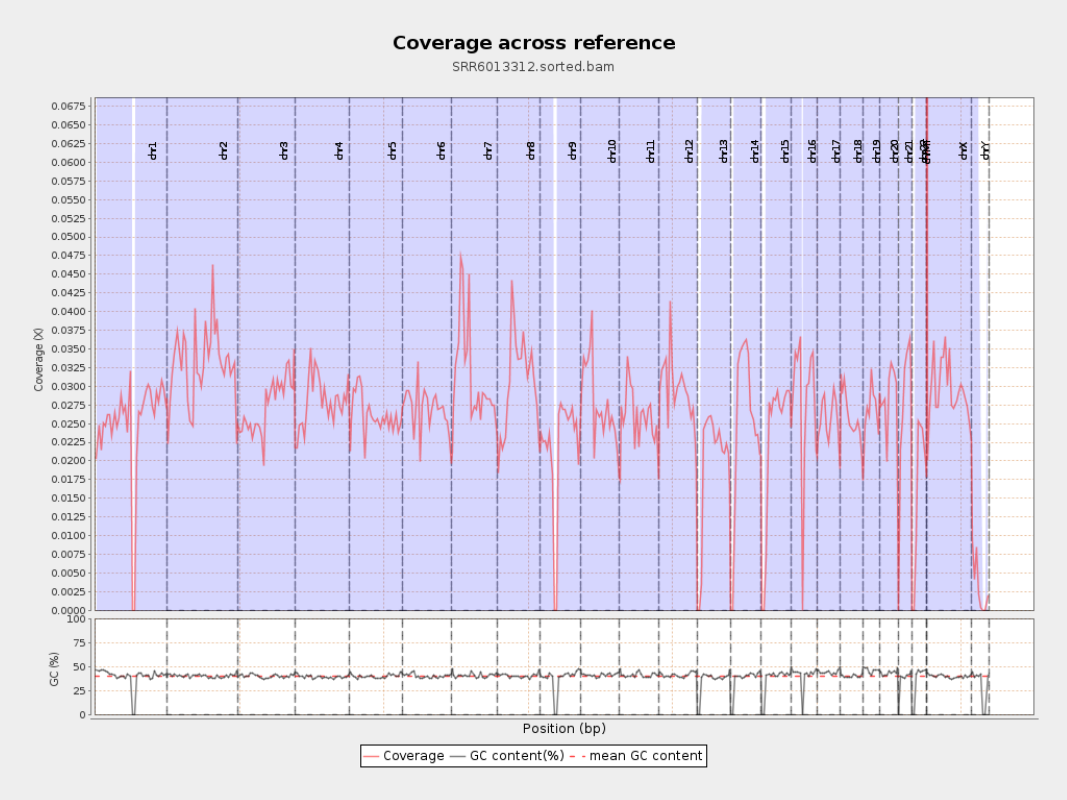
General error rate	0.71%
Mismatches	578,611
Insertions	5,537
Mapped reads with at least one insertion	0.43%
Deletions	20,040
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.2%

2.6. Chromosome stats

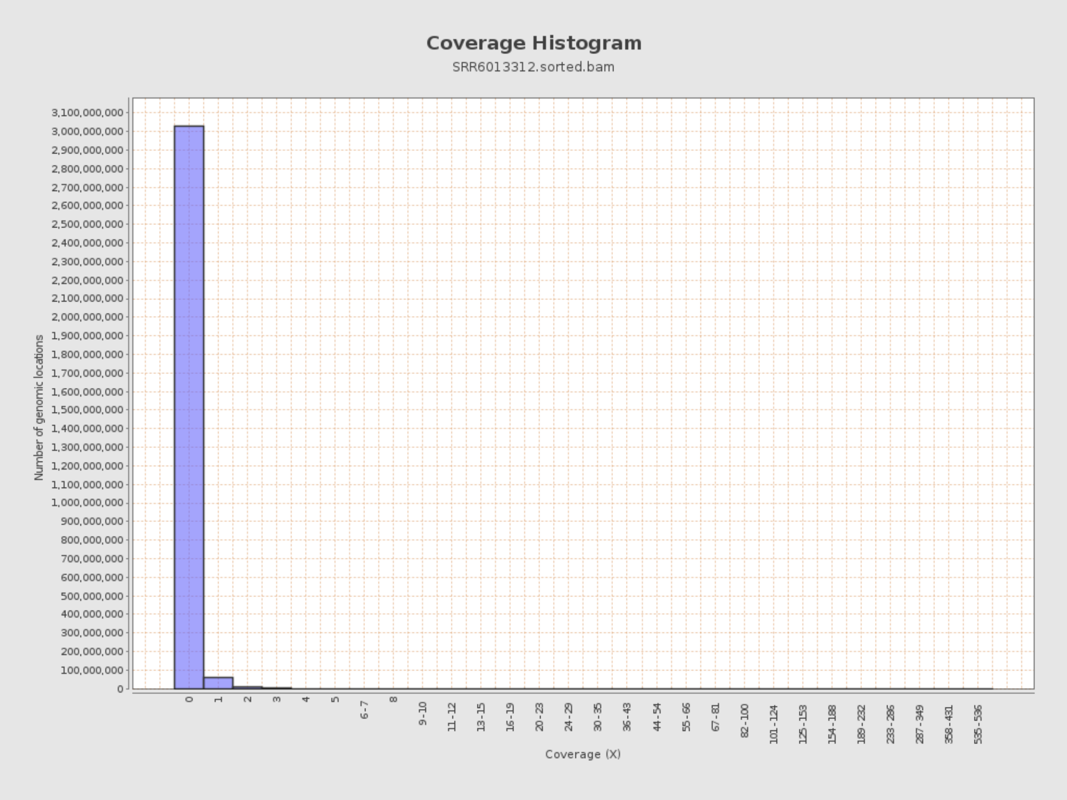
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6207145	0.0249	0.3111
chr2	243199373	8061272	0.0331	0.3318
chr3	198022430	5394112	0.0272	0.1914
chr4	191154276	5343833	0.028	0.1965
chr5	180915260	4749429	0.0263	0.188
chr6	171115067	4604470	0.0269	0.218
chr7	159138663	4976573	0.0313	0.3591

chr8	146364022	4506054	0.0308	0.3013
chr9	141213431	3048884	0.0216	0.2017
chr10	135534747	3770113	0.0278	0.2463
chr11	135006516	3518030	0.0261	0.2023
chr12	133851895	3984981	0.0298	0.2033
chr13	115169878	2239290	0.0194	0.1696
chr14	107349540	2668663	0.0249	0.1894
chr15	102531392	2315638	0.0226	0.1771
chr16	90354753	2496639	0.0276	0.1997
chr17	81195210	2090492	0.0257	0.1926
chr18	78077248	2021041	0.0259	0.3355
chr19	59128983	1590445	0.0269	0.2787
chr20	63025520	1783070	0.0283	0.1977
chr21	48129895	1322003	0.0275	0.1973
chr22	51304566	839192	0.0164	0.1461
chrMT	16571	211959	12.791	12.0693
chrX	155270560	4592412	0.0296	0.2063
chrY	59373566	182116	0.0031	0.0764

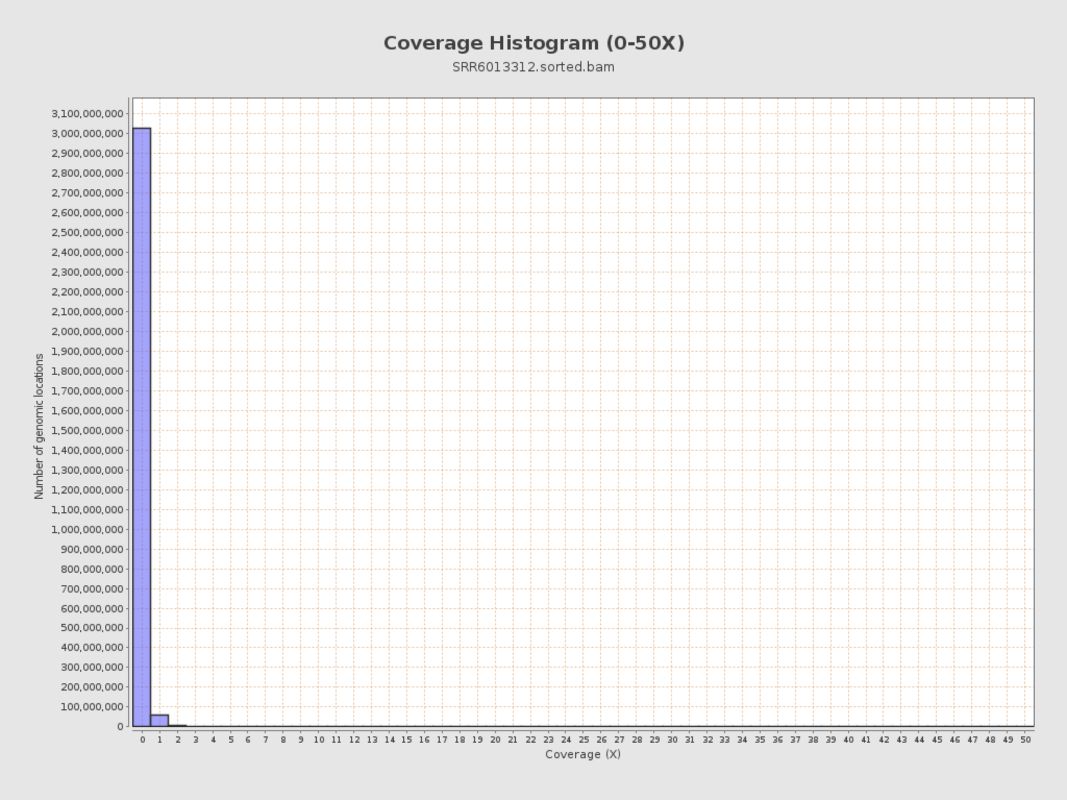
3. Results : Coverage across reference



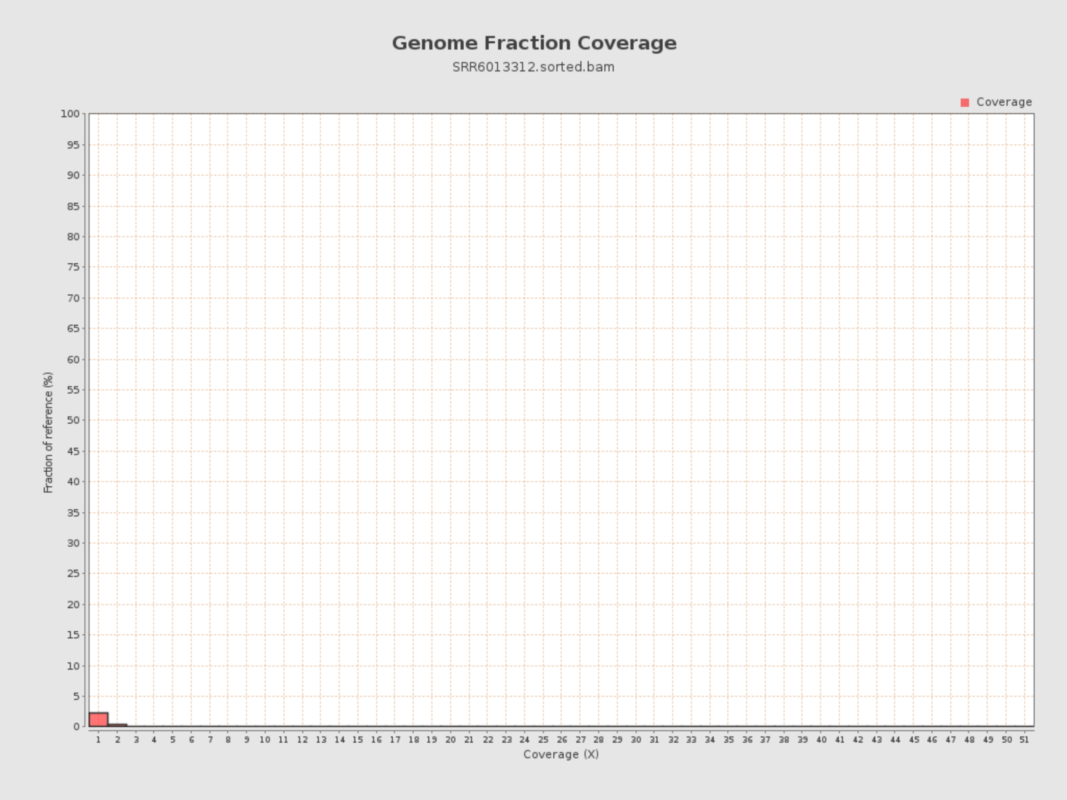
4. Results : Coverage Histogram



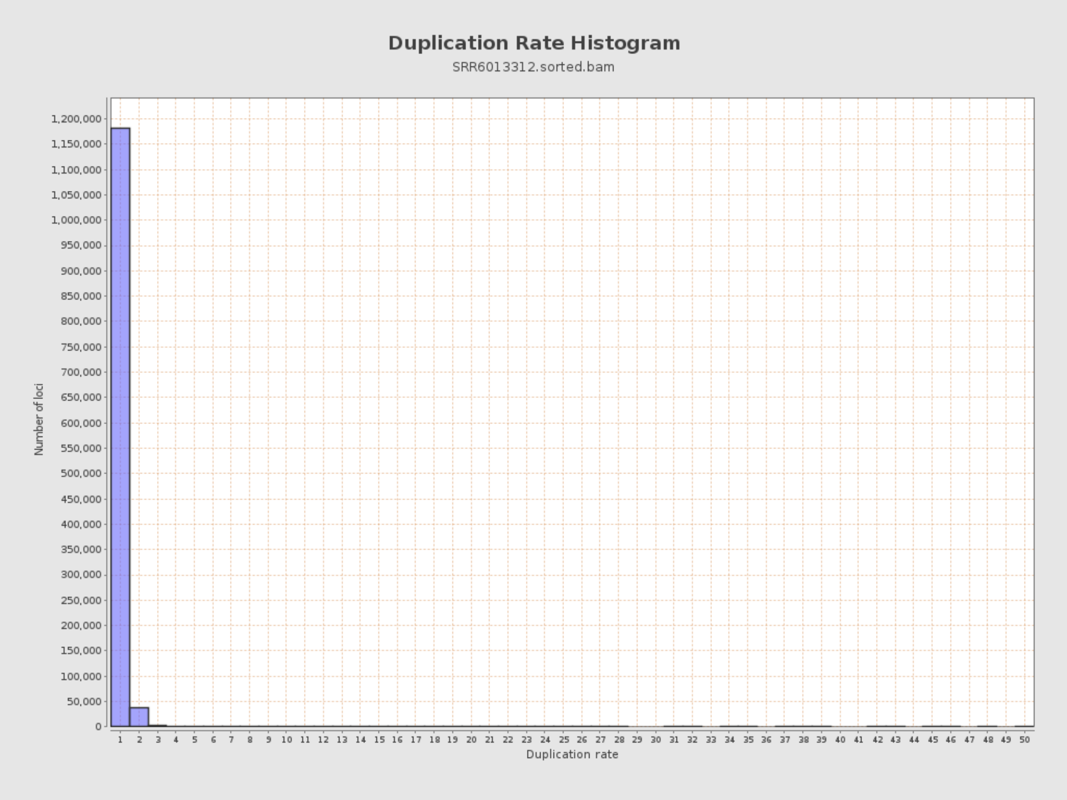
5. Results : Coverage Histogram (0-50X)



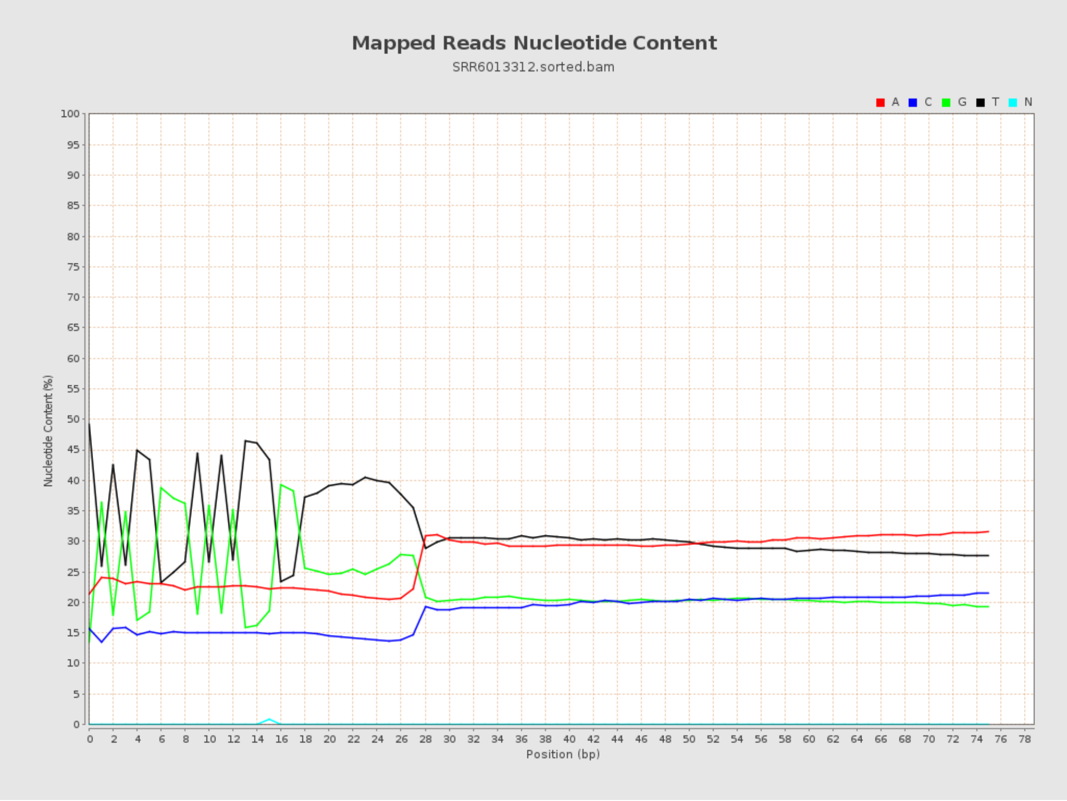
6. Results : Genome Fraction Coverage



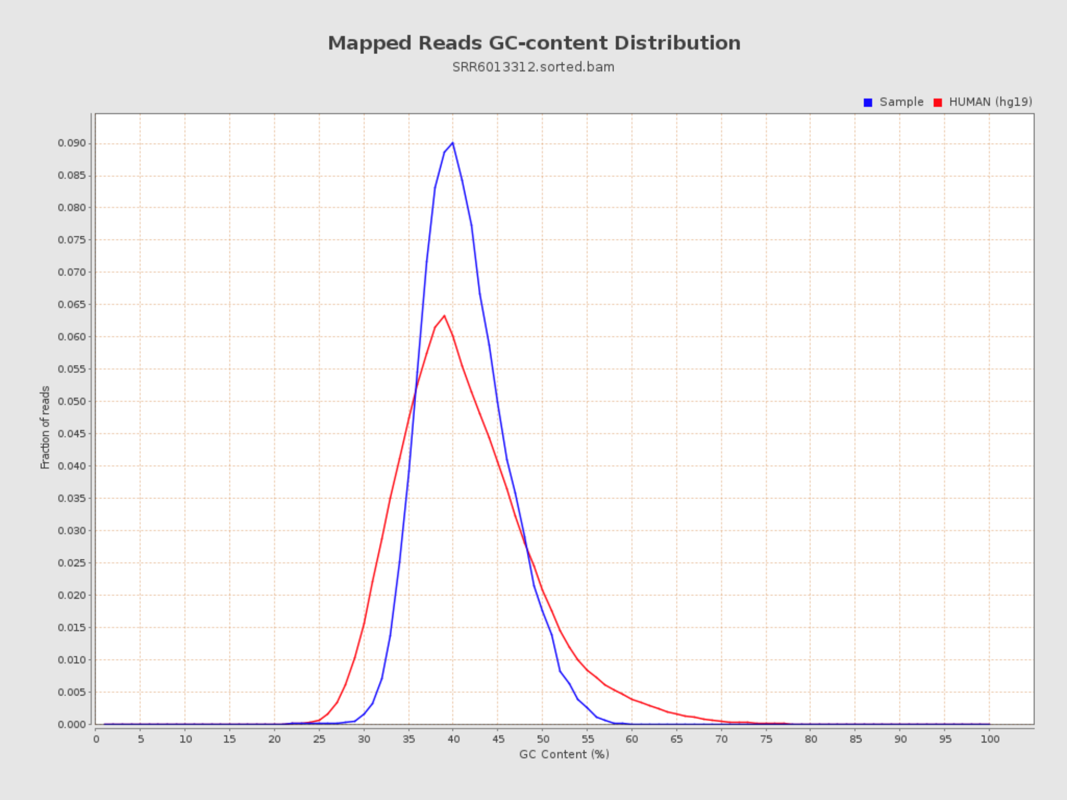
7. Results : Duplication Rate Histogram



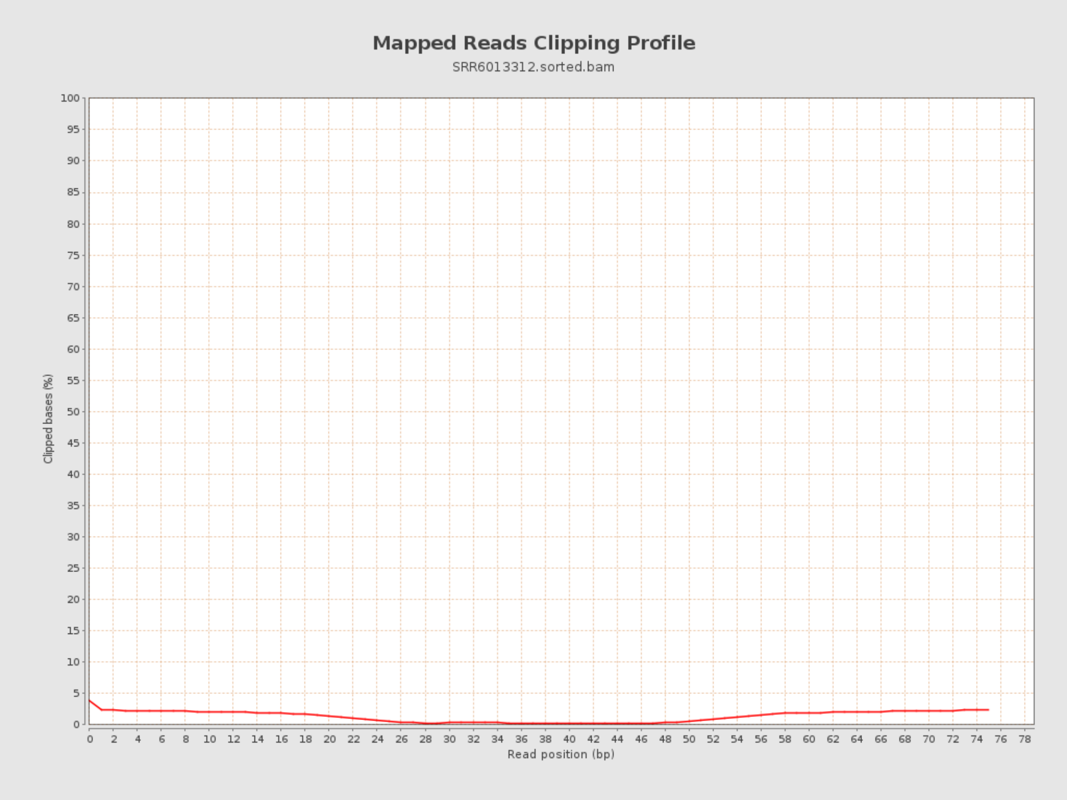
8. Results : Mapped Reads Nucleotide Content



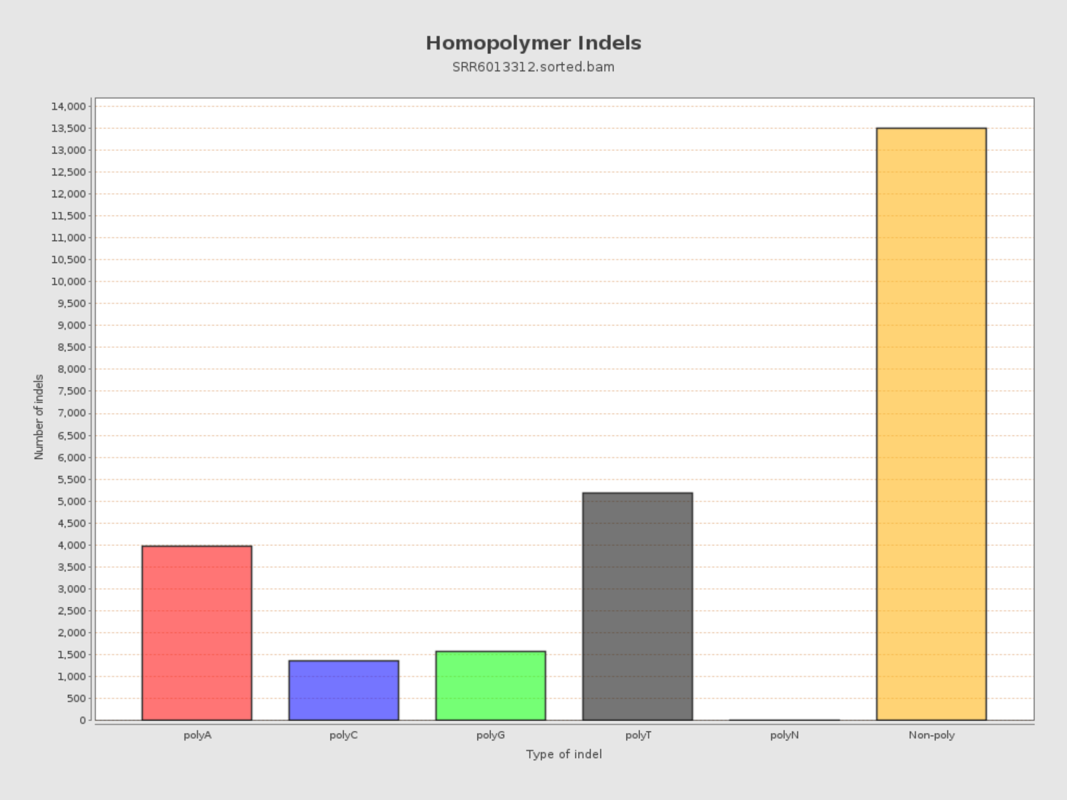
9. Results : Mapped Reads GC-content Distribution



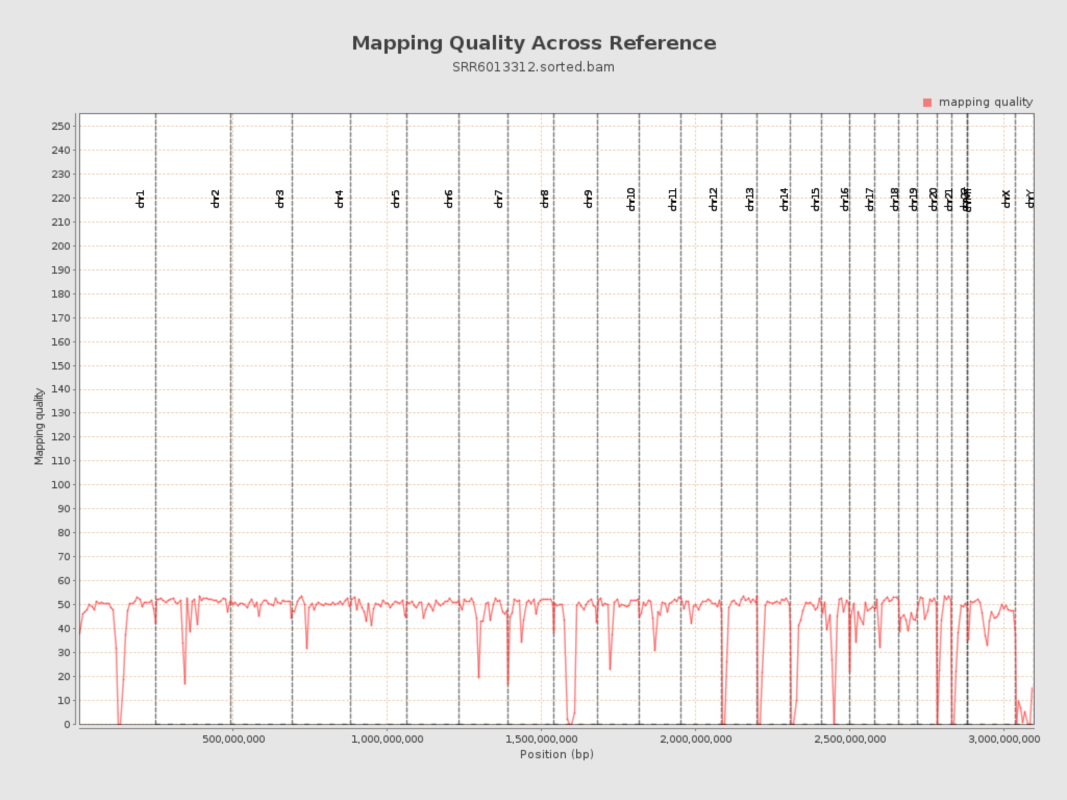
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram